

SEQUENCE LISTING

<110> Laus, Reiner
Vidovic, Damir
Graddis, Thomas

<120> Compositions and Methods for Dendritic
Cell-Based Immunotherapy

<130> 7636-0022.30

<140> Not Yet Assigned

<141> Filed Herewith

<150> US 60/193,504

<151> 2000-03-30

<160> 30

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 555

<212> PRT

<213> Artificial Sequence

<220>

<223> HER500 construct

<400> 1

Met	Arg	Ala	Ala	Pro	Leu	Leu	Leu	Ala	Arg	Ala	Ala	Ser	Leu	Ser	Leu
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Gly	Phe	Leu	Phe	Leu	Leu	Phe	Phe	Trp	Leu	Asp	Arg	Ser	Val	Leu	Ala
			20					25					30		
Lys	Glu	Leu	Ala	Arg	Gly	Ala	Ala	Ser	Thr	Gln	Val	Cys	Thr	Gly	Thr
		35					40					45			
Asp	Met	Lys	Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	Thr	His	Leu	Asp	Met
	50					55					60				
Leu	Arg	His	Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu	Glu
65					70					75					80
Leu	Thr	Tyr	Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile
			85						90					95	
Gln	Glu	Val	Gln	Gly	Tyr	Val	Leu	Ile	Ala	His	Asn	Gln	Val	Arg	Gln
			100						105					110	
Val	Pro	Leu	Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu
			115				120						125		
Asp	Asn	Tyr	Ala	Leu	Ala	Val	Leu	Asp	Asn	Gly	Asp	Pro	Leu	Asn	Asn
	130					135					140				
Thr	Thr	Pro	Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln
145					150					155					160
Leu	Arg	Ser	Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg
			165						170					175	
Asn	Pro	Gln	Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe
			180					185					190		
His	Lys	Asn	Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser

195	200	205
Arg Ala Cys His Pro Cys Ser	Pro Met Cys Lys Gly	Ser Arg Cys Trp
210	215	220
Gly Glu Ser Ser Glu Asp Cys	Gln Ser Leu Thr Arg Thr	Val Cys Ala
225	230	235
Gly Gly Cys Ala Arg Cys Lys	Gly Pro Leu Pro Thr Asp Cys	Cys His
245	250	255
Glu Gln Cys Ala Ala Gly Cys	Thr Gly Pro Lys His Ser Asp Cys	Leu
260	265	270
Ala Cys Leu His Phe Asn His	Ser Gly Ile Cys Glu Leu His	Cys Pro
275	280	285
Ala Leu Val Thr Tyr Asn Thr	Asp Thr Phe Glu Ser Met Pro	Asn Pro
290	295	300
Gly Gly Arg Tyr Thr Phe Gly	Ala Ser Cys Val Thr Ala Cys	Pro Tyr
305	310	315
Asn Tyr Leu Ser Thr Asp Val	Gly Ser Gly Ala Gly Gly Met	Val His
325	330	335
His Arg His Arg Ser Ser Ser	Thr Arg Ser Gly Gly Gly Asp	Leu Thr
340	345	350
Leu Gly Leu Glu Pro Ser Glu	Glu Glu Ala Pro Arg Ser Pro	Leu Ala
355	360	365
Pro Ser Glu Gly Ala Gly Ser	Asp Val Phe Asp Gly Asp Leu	Gly Met
370	375	380
Gly Ala Ala Lys Gly Leu Gln	Ser Leu Pro Thr His Asp Pro	Ser Pro
385	390	395
Leu Gln Arg Tyr Ser Glu Asp	Pro Thr Val Pro Leu Pro Ser	Glu Thr
405	410	415
Asp Gly Tyr Val Ala Pro Leu	Thr Cys Ser Pro Gln Pro Glu	Tyr Val
420	425	430
Asn Gln Pro Asp Val Arg Pro	Gln Pro Pro Ser Pro Arg Glu	Gly Pro
435	440	445
Leu Pro Ala Ala Arg Pro Ala	Gly Ala Thr Leu Glu Arg Ala	Lys Thr
450	455	460
Leu Ser Pro Gly Lys Asn Gly	Val Val Lys Asp Val Phe Ala	Phe Gly
465	470	475
Gly Ala Val Glu Asn Pro Glu	Tyr Leu Thr Pro Gln Gly Gly	Ala Ala
485	490	495
Pro Gln Pro His Pro Pro Pro	Ala Phe Ser Pro Ala Phe Asp	Asn Leu
500	505	510
Tyr Tyr Trp Asp Gln Asp Pro	Pro Glu Arg Gly Ala Pro Ser	Thr
515	520	525
Phe Lys Gly Thr Pro Thr Ala	Glu Asn Pro Glu Tyr Leu Gly	Leu Asp
530	535	540
Val Pro Ala Ala Ala His His	His His His His His	
545	550	555

<210> 2

<211> 690

<212> PRT

<213> Artificial Sequence

<220>

<223> HER500-hGM-CSF construct

<400> 2

Met Arg Ala Ala Pro Leu Leu Leu Ala Arg Ala Ala Ser Leu Ser Leu
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Gly	Phe	Leu	Phe	Leu	Leu	Phe	Phe	Trp	Leu	Asp	Arg	Ser	Val	Leu	Ala
		20						25					30		
Lys	Glu	Leu	Ala	Arg	Gly	Ala	Ala	Ser	Thr	Gln	Val	Cys	Thr	Gly	Thr
		35					40					45			
Asp	Met	Lys	Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	Thr	His	Leu	Asp	Met
	50					55					60				
Leu	Arg	His	Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu	Glu
65					70					75					80
Leu	Thr	Tyr	Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile
			85						90					95	
Gln	Glu	Val	Gln	Gly	Tyr	Val	Leu	Ile	Ala	His	Asn	Gln	Val	Arg	Gln
			100					105					110		
Val	Pro	Leu	Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu
		115					120					125			
Asp	Asn	Tyr	Ala	Leu	Ala	Val	Leu	Asp	Asn	Gly	Asp	Pro	Leu	Asn	Asn
	130					135					140				
Thr	Thr	Pro	Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln
145					150					155					160
Leu	Arg	Ser	Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg
			165					170						175	
Asn	Pro	Gln	Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe
		180						185					190		
His	Lys	Asn	Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser
		195					200					205			
Arg	Ala	Cys	His	Pro	Cys	Ser	Pro	Met	Cys	Lys	Gly	Ser	Arg	Cys	Trp
	210					215					220				
Gly	Glu	Ser	Ser	Glu	Asp	Cys	Gln	Ser	Leu	Thr	Arg	Thr	Val	Cys	Ala
225					230					235					240
Gly	Gly	Cys	Ala	Arg	Cys	Lys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His
			245					250						255	
Glu	Gln	Cys	Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu
			260					265					270		
Ala	Cys	Leu	His	Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro
		275					280					285			
Ala	Leu	Val	Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu	Ser	Met	Pro	Asn	Pro
	290					295					300				
Glu	Gly	Arg	Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro	Tyr
305					310					315					320
Asn	Tyr	Leu	Ser	Thr	Asp	Val	Gly	Ser	Gly	Ala	Gly	Gly	Met	Val	His
			325					330						335	
His	Arg	His	Arg	Ser	Ser	Ser	Thr	Arg	Ser	Gly	Gly	Gly	Asp	Leu	Thr
		340						345					350		
Leu	Gly	Leu	Glu	Pro	Ser	Glu	Glu	Glu	Ala	Pro	Arg	Ser	Pro	Leu	Ala
		355					360					365			
Pro	Ser	Glu	Gly	Ala	Gly	Ser	Asp	Val	Phe	Asp	Gly	Asp	Leu	Gly	Met
	370					375					380				
Gly	Ala	Ala	Lys	Gly	Leu	Gln	Ser	Leu	Pro	Thr	His	Asp	Pro	Ser	Pro
385					390					395					400
Leu	Gln	Arg	Tyr	Ser	Glu	Asp	Pro	Thr	Val	Pro	Leu	Pro	Ser	Glu	Thr
			405						410					415	
Asp	Gly	Tyr	Val	Ala	Pro	Leu	Thr	Cys	Ser	Pro	Gln	Pro	Glu	Tyr	Val
		420						425					430		
Asn	Gln	Pro	Asp	Val	Arg	Pro	Gln	Pro	Pro	Ser	Pro	Arg	Glu	Gly	Pro
		435					440					445			
Leu	Pro	Ala	Ala	Arg	Pro	Ala	Gly	Ala	Thr	Leu	Glu	Arg	Ala	Lys	Thr
	450					455					460				
Leu	Ser	Pro	Gly	Lys	Asn	Gly	Val	Val	Lys	Asp	Val	Phe	Ala	Phe	Gly

465		470		475		480									
Gly	Ala	Val	Glu	Asn	Pro	Glu	Tyr	Leu	Thr	Pro	Gln	Gly	Gly	Ala	Ala
				485					490					495	
Pro	Gln	Pro	His	Pro	Pro	Pro	Ala	Phe	Ser	Pro	Ala	Phe	Asp	Asn	Leu
			500					505					510		
Tyr	Tyr	Trp	Asp	Gln	Asp	Pro	Pro	Glu	Arg	Gly	Ala	Pro	Pro	Ser	Thr
		515					520					525			
Phe	Lys	Gly	Thr	Pro	Thr	Ala	Glu	Asn	Pro	Glu	Tyr	Leu	Gly	Leu	Asp
	530					535					540				
Val	Pro	Ala	Ala	Ala	Pro	Ala	Arg	Ser	Pro	Ser	Pro	Ser	Thr	Gln	Pro
545					550					555					560
Trp	Glu	His	Val	Asn	Ala	Ile	Gln	Glu	Ala	Arg	Arg	Leu	Leu	Asn	Leu
				565					570					575	
Ser	Arg	Asp	Thr	Ala	Ala	Glu	Met	Asn	Glu	Thr	Val	Glu	Val	Ile	Ser
			580					585					590		
Glu	Met	Phe	Asp	Leu	Gln	Glu	Pro	Thr	Cys	Leu	Gln	Thr	Arg	Leu	Glu
		595				600						605			
Leu	Tyr	Lys	Gln	Gly	Leu	Arg	Gly	Ser	Leu	Thr	Lys	Leu	Lys	Gly	Pro
	610					615					620				
Leu	Thr	Met	Met	Ala	Ser	His	Tyr	Lys	Gln	His	Cys	Pro	Pro	Thr	Pro
625					630					635					640
Glu	Thr	Ser	Cys	Ala	Thr	Gln	Ile	Ile	Thr	Phe	Glu	Ser	Phe	Lys	Glu
				645					650					655	
Asn	Leu	Lys	Asp	Phe	Leu	Leu	Val	Ile	Pro	Phe	Asp	Cys	Trp	Glu	Pro
			660					665					670		
Val	Gln	Glu	Gly	Ala	Pro	Pro	Pro	Pro	Ala	Ala	Ala	His	His	His	His
		675					680					685			
His	His														
	690														

<210> 3
 <211> 564
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HER500* construct

<400> 3
Met Arg Ala Ala Pro Leu Leu Leu Ala Arg Ala Ala Ser Leu Ser Leu
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Gly Phe Leu Phe Leu Leu Phe Phe Trp Leu Asp Arg Ser Val Leu Ala
20 25 30
Lys Glu Leu Ala Arg Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr
35 40 45
Asp Met Lys Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met
50 55 60
Leu Arg His Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu
65 70 75 80
Leu Thr Tyr Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile
85 90 95
Gln Glu Val Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln
100 105 110
Val Pro Leu Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu
115 120 125
Asp Asn Tyr Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn
130 135 140

Thr	Thr	Pro	Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln
145					150					155					160
Leu	Arg	Ser	Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg
				165					170					175	
Asn	Pro	Gln	Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe
			180					185					190		
His	Lys	Asn	Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser
		195					200					205			
Arg	Ala	Cys	His	Pro	Cys	Ser	Pro	Met	Cys	Lys	Gly	Ser	Arg	Cys	Trp
	210					215					220				
Gly	Glu	Ser	Ser	Glu	Asp	Cys	Gln	Ser	Leu	Thr	Arg	Thr	Val	Cys	Ala
225					230					235					240
Gly	Gly	Cys	Ala	Arg	Cys	Lys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His
				245					250					255	
Glu	Gln	Cys	Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu
			260					265					270		
Ala	Cys	Leu	His	Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro
		275					280					285			
Ala	Leu	Val	Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu	Ser	Met	Pro	Asn	Pro
	290					295					300				
Glu	Gly	Arg	Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro	Tyr
305					310					315					320
Asn	Tyr	Leu	Ser	Thr	Asp	Val	Gly	Ser	Ala	Ser	Ile	Ile	Asn	Phe	Glu
				325					330					335	
Lys	Leu	Gly	Ala	Gly	Gly	Met	Val	His	His	Arg	His	Arg	Ser	Ser	Ser
			340					345					350		
Thr	Arg	Ser	Gly	Gly	Gly	Asp	Leu	Thr	Leu	Gly	Leu	Glu	Pro	Ser	Glu
		355					360					365			
Glu	Glu	Ala	Pro	Arg	Ser	Pro	Leu	Ala	Pro	Ser	Glu	Gly	Ala	Gly	Ser
	370					375					380				
Asp	Val	Phe	Asp	Gly	Asp	Leu	Gly	Met	Gly	Ala	Ala	Lys	Gly	Leu	Gln
385					390					395					400
Ser	Leu	Pro	Thr	His	Asp	Pro	Ser	Pro	Leu	Gln	Arg	Tyr	Ser	Glu	Asp
				405					410					415	
Pro	Thr	Val	Pro	Leu	Pro	Ser	Glu	Thr	Asp	Gly	Tyr	Val	Ala	Pro	Leu
		420					425						430		
Thr	Cys	Ser	Pro	Gln	Pro	Glu	Tyr	Val	Asn	Gln	Pro	Asp	Val	Arg	Pro
		435					440					445			
Gln	Pro	Pro	Ser	Pro	Arg	Glu	Gly	Pro	Leu	Pro	Ala	Ala	Arg	Pro	Ala
	450					455					460				
Gly	Ala	Thr	Leu	Glu	Arg	Ala	Lys	Thr	Leu	Ser	Pro	Gly	Lys	Asn	Gly
465					470					475					480
Val	Val	Lys	Asp	Val	Phe	Ala	Phe	Gly	Gly	Ala	Val	Glu	Asn	Pro	Glu
				485					490					495	
Tyr	Leu	Thr	Pro	Gln	Gly	Gly	Ala	Ala	Pro	Gln	Pro	His	Pro	Pro	Pro
			500					505					510		
Ala	Phe	Ser	Pro	Ala	Phe	Asp	Asn	Leu	Tyr	Tyr	Trp	Asp	Gln	Asp	Pro
		515					520					525			
Pro	Glu	Arg	Gly	Ala	Pro	Pro	Ser	Thr	Phe	Lys	Gly	Thr	Pro	Thr	Ala
	530					535					540				
Glu	Asn	Pro	Glu	Tyr	Leu	Gly	Leu	Asp	Val	Pro	Ala	Ala	Ala	His	His
545					550					555					560
His	His	His	His												

<210> 4

<211> 697

<212> PRT

<213> Artificial Sequence

<220>

<223> HER500*-rGM-CSF construct

<400> 4

Met	Arg	Ala	Ala	Pro	Leu	Leu	Leu	Ala	Arg	Ala	Ala	Ser	Leu	Ser	Leu	
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Gly	Phe	Leu	Phe	Leu	Leu	Phe	Phe	Trp	Leu	Asp	Arg	Ser	Val	Leu	Ala	
			20					25					30			
Lys	Glu	Leu	Ala	Arg	Gly	Ala	Ala	Ser	Thr	Gln	Val	Cys	Thr	Gly	Thr	
		35				40						45				
Asp	Met	Lys	Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	Thr	His	Leu	Asp	Met	
	50					55				60						
Leu	Arg	His	Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu	Glu	
65				70					75					80		
Leu	Thr	Tyr	Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile	
			85					90						95		
Gln	Glu	Val	Gln	Gly	Tyr	Val	Leu	Ile	Ala	His	Asn	Gln	Val	Arg	Gln	
			100					105					110			
Val	Pro	Leu	Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	
		115				120						125				
Asp	Asn	Tyr	Ala	Leu	Ala	Val	Leu	Asp	Asn	Gly	Asp	Pro	Leu	Asn	Asn	
	130					135					140					
Thr	Thr	Pro	Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln	
145					150					155					160	
Leu	Arg	Ser	Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg	
				165				170						175		
Asn	Pro	Gln	Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe	
			180				185						190			
His	Lys	Asn	Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser	
	195					200						205				
Arg	Ala	Cys	His	Pro	Cys	Ser	Pro	Met	Cys	Lys	Gly	Ser	Arg	Cys	Trp	
	210				215						220					
Gly	Glu	Ser	Ser	Glu	Asp	Cys	Gln	Ser	Leu	Thr	Arg	Thr	Val	Cys	Ala	
225				230						235					240	
Gly	Gly	Cys	Ala	Arg	Cys	Lys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His	
			245					250						255		
Glu	Gln	Cys	Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	
		260					265						270			
Ala	Cys	Leu	His	Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro	
	275					280						285				
Ala	Leu	Val	Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu	Ser	Met	Pro	Asn	Pro	
	290					295					300					
Glu	Gly	Arg	Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro	Tyr	
305				310						315					320	
Asn	Tyr	Leu	Ser	Thr	Asp	Val	Gly	Ser	Ala	Ser	Ile	Ile	Asn	Phe	Glu	
				325				330						335		
Lys	Leu	Gly	Ala	Gly	Gly	Met	Val	His	His	Arg	His	Arg	Ser	Ser	Ser	
		340					345						350			
Thr	Arg	Ser	Gly	Gly	Gly	Asp	Leu	Thr	Leu	Gly	Leu	Glu	Pro	Ser	Glu	
	355					360						365				
Glu	Glu	Ala	Pro	Arg	Ser	Pro	Leu	Ala	Pro	Ser	Glu	Gly	Ala	Gly	Ser	
	370				375						380					
Asp	Val	Phe	Asp	Gly	Asp	Leu	Gly	Met	Gly	Ala	Ala	Lys	Gly	Leu	Gln	
385				390						395					400	

Ser	Leu	Pro	Thr	His	Asp	Pro	Ser	Pro	Leu	Gln	Arg	Tyr	Ser	Glu	Asp
				405					410					415	
Pro	Thr	Val	Pro	Leu	Pro	Ser	Glu	Thr	Asp	Gly	Tyr	Val	Ala	Pro	Leu
			420					425					430		
Thr	Cys	Ser	Pro	Gln	Pro	Glu	Tyr	Val	Asn	Gln	Pro	Asp	Val	Arg	Pro
		435					440					445			
Gln	Pro	Pro	Ser	Pro	Arg	Glu	Gly	Pro	Leu	Pro	Ala	Ala	Arg	Pro	Ala
	450					455					460				
Gly	Ala	Thr	Leu	Glu	Arg	Ala	Lys	Thr	Leu	Ser	Pro	Gly	Lys	Asn	Gly
465					470					475					480
Val	Val	Lys	Asp	Val	Phe	Ala	Phe	Gly	Gly	Ala	Val	Glu	Asn	Pro	Glu
			485					490						495	
Tyr	Leu	Thr	Pro	Gln	Gly	Gly	Ala	Ala	Pro	Gln	Pro	His	Pro	Pro	Pro
			500					505					510		
Ala	Phe	Ser	Pro	Ala	Phe	Asp	Asn	Leu	Tyr	Tyr	Trp	Asp	Gln	Asp	Pro
		515					520					525			
Pro	Glu	Arg	Gly	Ala	Pro	Pro	Ser	Thr	Phe	Lys	Gly	Thr	Pro	Thr	Ala
	530					535					540				
Glu	Asn	Pro	Glu	Tyr	Leu	Gly	Leu	Asp	Val	Pro	Ala	Ala	Ala	Pro	Thr
545					550					555					560
Arg	Ser	Pro	Asn	Pro	Val	Thr	Arg	Pro	Trp	Lys	His	Val	Asp	Ala	Ile
			565					570					575		
Lys	Glu	Ala	Leu	Ser	Leu	Leu	Asn	Asp	Met	Arg	Ala	Leu	Glu	Asn	Glu
		580					585					590			
Lys	Asn	Glu	Asp	Val	Asp	Ile	Ile	Ser	Asn	Glu	Phe	Ser	Ile	Gln	Arg
		595				600						605			
Pro	Thr	Cys	Val	Gln	Thr	Arg	Leu	Lys	Leu	Tyr	Lys	Gln	Gly	Leu	Arg
	610					615					620				
Gly	Asn	Leu	Thr	Lys	Leu	Asn	Gly	Ala	Leu	Thr	Met	Ile	Ala	Ser	His
625					630					635					640
Tyr	Gln	Thr	Asn	Cys	Pro	Pro	Thr	Pro	Glu	Thr	Asp	Cys	Glu	Ile	Glu
			645					650					655		
Val	Thr	Thr	Phe	Glu	Asp	Phe	Ile	Lys	Asn	Leu	Lys	Gly	Phe	Leu	Phe
			660				665					670			
Asp	Ile	Pro	Phe	Asp	Cys	Trp	Lys	Pro	Val	Gln	Lys	Gly	Ala	Pro	Pro
	675					680						685			
Pro	Pro	Ala	His	His	His	His	His	His							
	690				695										

<210> 5

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> HER300*-rGM-CSF construct

<400> 5

Met	Arg	Ala	Ala	Pro	Leu	Leu	Leu	Ala	Arg	Ala	Ala	Ser	Leu	Ser	Leu
1				5				10					15		
Gly	Phe	Leu	Phe	Leu	Leu	Phe	Phe	Trp	Leu	Asp	Arg	Ser	Val	Leu	Ala
		20					25					30			
Lys	Glu	Leu	Ala	Arg	Gly	Ala	Ala	Ser	Thr	Gln	Val	Cys	Thr	Gly	Thr
	35					40					45				
Asp	Met	Lys	Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	Thr	His	Leu	Asp	Met
50					55					60					
Leu	Arg	His	Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu	Glu

65					70					75				80
Leu	Thr	Tyr	Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp Ile
				85					90					95
Gln	Glu	Val	Gln	Gly	Tyr	Val	Leu	Ile	Ala	His	Asn	Gln	Val	Arg Gln
			100					105					110	
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His	Lys	Asn	Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg Ser
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Ala	Cys	Leu	His	Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys Pro
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Tyr	Lys	Gln	Gly	Leu	Arg	Gly	Asn	Leu	Thr	Lys	Leu	Asn	Gly	Ala Leu
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Thr	Asp	Cys	Glu	Ile	Glu	Val	Thr	Thr	Phe	Glu	Asp	Phe	Ile	Lys Asn
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Leu	Lys	Gly	Phe	Leu	Phe	Asp	Ile	Pro	Phe	Asp	Cys	Trp	Lys	Pro Val
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<210> 6

<211> 1665

<212> DNA

<213> Artificial Sequence

<220>

<223> HER500 construct

<400> 6

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<210> 7

<211> 2070

<212> DNA

<213> Artificial Sequence

<220>

<223> HER500-hGM-CSF construct

<400> 7

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<210> 8

<211> 1692

<212> DNA

<213> Artificial Sequence

<220>

<223> HER500* construct

<400> 8

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<210> 9
<211> 2091
<212> DNA
<213> Artificial Sequence

<220>
<223> HER500*-rGM-CSF construct

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<211> 1437
<212> DNA
<213> Artificial Sequence

<220>
<223> HER300*-rGM-CSF construct

<400> 10

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 <212> PRT
 <213> Homo sapiens

<400> 11
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<210> 12
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 <212> PRT
 <213> Homo sapiens

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<210> 13
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<223> linker

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<210> 15

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> C-terminal sequence of HER500 and HER500* constructs

<400> 15

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5

<210> 16

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> C-terminal sequence of HER500-hGM-CSF construct

<400> 16

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5

10

15

<210> 17

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> C-terminal sequence of HER500* and HER300* rat GM-CSF constructs

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<210> 18

<211> 127

<212> PRT

<213> Homo sapiens

<400> 18

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5

10

15

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20

25

30

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Ala	Thr	Gln	Ile	Ile	Thr	Phe	Glu	Ser	Phe	Lys	Glu	Asn	Leu	Lys	Asp
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<210> 19
 <211> 381
 <212> DNA
 <213> Homo sapiens

<400> 19	gcacccgccc gctcgcccag cccagcagc cagccctggg agcatgtgaa tgccatccag	60
	gagggccggc gtctcctgaa cctgagtaga gacactgctg ctgagatgaa tgaaacagta	120
	gaagtcatct cagaaatgtt tgacctccag gagccgacct gcctacagac ccgcctggag	180
	ctgtacaagc agggcctgcg gggcagcctc accaagctca agggcccctt gaccatgatg	240
	gccagccact acaagcagca ctgccctcca accccggaaa cttcctgtgc aaccagact	300
	atcacctttg aaagtttcaa agagaacctg aaggactttc tgcttgatcat cccctttgac	360
	tgctgggagc cagtccagga g	381

<210> 20
 <211> 127
 <212> PRT
 <213> Rattus norvegicus

<400> 20	Ala Pro Thr Arg Ser Pro Asn Pro Val Thr Arg Pro Trp Lys His Val
	1 5 10 15
Asp	Ala Ile Lys Glu Ala Leu Ser Leu Leu Asn Asp Met Arg Ala Leu
	20 25 30
Glu	Asn Glu Lys Asn Glu Asp Val Asp Ile Ile Ser Asn Glu Phe Ser
	35 40 45
Ile	Gln Arg Pro Thr Cys Val Gln Thr Arg Leu Lys Leu Tyr Lys Gln
	50 55 60
Gly	Leu Arg Gly Asn Leu Thr Lys Leu Asn Gly Ala Leu Thr Met Ile
65	
Ala	Ser His Tyr Gln Thr Asn Cys Pro Pro Thr Pro Glu Thr Asp Cys
	85 90 95
Glu	Ile Glu Val Thr Thr Phe Glu Asp Phe Ile Lys Asn Leu Lys Gly
	100 105 110
Phe	Leu Phe Asp Ile Pro Phe Asp Cys Trp Lys Pro Val Gln Lys
	115 120 125

<210> 21
 <211> 381
 <212> DNA
 <213> Rattus norvegicus

<400> 21	gcacccaccc gctcacccaa ccctgtcacc cggccctgga agcatgtaga tgccatcaaa	60
----------	---	----

gaagctctga gctcctctaaa tgacatgcgt gctctggaga acgaaaagaa cgaagacgta	120
gacatcatct ctaatgagtt ctccatccag aggccgacat gtgtgcagac ccgcctgaag	180
ctatacaagc aggggtctacg gggcaacctc accaaactca atggcgctt gaccatgata	240
gccagccact accagacgaa ctgccctcca accccggaaa ctgactgtga aatagaagtc	300
accacctttg aggatttcac aaagaacctt aaaggctttc tgtttgatat cccttttgac	360
tgctggaagc cggtccagaa a	381

<210> 22
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> OVA-derived immunodominant octapeptide

<400> 22
 Ser Ile Ile Asn Phe Glu Lys Leu
 1 5

<210> 23
 <211> 289
 <212> PRT
 <213> Homo sapiens

<400> 23
 Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys Leu Arg Leu Pro Ala
 1 5 10 15
 Ser Pro Glu Thr His Leu Asp Met Leu Arg His Leu Tyr Gln Gly Cys
 20 25 30
 Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr Leu Pro Thr Asn Ala
 35 40 45
 Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val Gln Gly Tyr Val Leu
 50 55 60
 Ile Ala His Asn Gln Val Arg Gln Val Pro Leu Gln Arg Leu Arg Ile
 65 70 75 80
 Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr Ala Leu Ala Val Leu
 85 90 95
 Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro Val Thr Gly Ala Ser
 100 105 110
 Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser Leu Thr Glu Ile Leu
 115 120 125
 Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln Leu Cys Tyr Gln Asp
 130 135 140
 Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn Asn Gln Leu Ala Leu
 145 150 155 160
 Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys His Pro Cys Ser Pro
 165 170 175
 Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser Ser Glu Asp Cys Gln
 180 185 190
 Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys Ala Arg Cys Lys Gly
 195 200 205
 Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys Ala Ala Gly Cys Thr
 210 215 220
 Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu His Phe Asn His Ser
 225 230 235 240
 Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val Thr Tyr Asn Thr Asp
 245 250 255

Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg Tyr Thr Phe Gly Ala
 260 265 270
 Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu Ser Thr Asp Val Gly
 275 280 285
 Ser

<210> 24
 <211> 867
 <212> DNA
 <213> Homo sapiens

<400> 24
 agcaccacaag tgtgcaccgg cacagacatg aagctgcggc tccctgccag tcccgagacc 60
 cacctggaca tgctccgcca cctctaccag ggctgccagg tgggtgcaggg aaacctggaa 120
 ctcacctacc tgcccaccaa tgccagcctg tccttcctgc aggatatcca ggaggtgcag 180
 ggctacgtgc tcatcgctca caaccaagtg aggcaggtcc cactgcagag gctgcggatt 240
 gtgcgaggca cccagctctt tgaggacaac tatgccctgg ccgtgctaga caatggagac 300
 ccgctgaaca ataccacccc tgtcacaggg gcctccccag gaggcctgcg ggagctgcag 360
 cttcgaagcc tcacagagat cttgaaagga ggggtcttga tccagcggaa cccccagctc 420
 tgctaccagg acacgatttt gtggaaggac atcttcacaca agaacaacca gctggctctc 480
 acactgatag acaccaaccg ctctcggggc tgccaccctt gttctccgat gtgtaagggc 540
 tcccgtctgt ggggagagag ttctgaggat tgtcagagcc tgacgcgcac tgtctgtgcc 600
 ggtggctgtg cccgctgcaa ggggccactg cccactgact gctgccatga gcagtgtgct 660
 gccggctgca cgggccccaa gcactctgac tgccctggct gcctccactt caaccacagt 720
 ggcattctgt agctgcactg cccagccctg gtcacctaca acacagacac gtttgagtcc 780
 atgcccaatc ccgagggcgg gtatacatte ggcgccagct gtgtgactgc ctgtccctac 840
 aactaccttt ctacggacgt gggatcc 867

<210> 25
 <211> 217
 <212> PRT
 <213> Homo sapiens

<400> 25
 Gly Ala Gly Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg
 1 5 10 15
 Ser Gly Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu
 20 25 30
 Ala Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val
 35 40 45
 Phe Asp Gly Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln Ser Leu
 50 55 60
 Pro Thr His Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr
 65 70 75 80
 Val Pro Leu Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu Thr Cys
 85 90 95
 Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro
 100 105 110
 Pro Ser Pro Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala
 115 120 125
 Thr Leu Glu Arg Ala Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val
 130 135 140
 Lys Asp Val Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu
 145 150 155 160
 Thr Pro Gln Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro Ala Phe
 165 170 175

Ser Pro Ala Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu
 180 185 190
 Arg Gly Ala Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn
 195 200 205
 Pro Glu Tyr Leu Gly Leu Asp Val Pro
 210 215

<210> 26
 <211> 651
 <212> DNA
 <213> Homo sapiens

<400> 26
 ggcgctgggg gcatgggtcca ccacaggcac cgcagctcat ctaccaggag tggcgggtggg 60
 gacctgacac tagggctgga gccctctgaa gaggaggccc ccaggtctcc actggcaccc 120
 tccgaagggg ctgggtccga tgtatttgat ggtgacctgg gaatgggggc agccaagggg 180
 ctgcaaagcc tccccacaca tgaccccagc cctctacagc ggtacagtga ggaccccaca 240
 gtacccctgc cctctgagac tgatgggtac gttgcccccc tgacctgcag cccccagcct 300
 gaatatgtga accagccaga tgttcggccc cagccccctt cgccccgaga gggccctctg 360
 cctgctgccc gacctgctgg tgccactctg gaaagggcca agactctctc cccagggaag 420
 aatgggggtcg tcaaagacgt ttttgccctt ggggggtgccg tggagaaccc cgagtacttg 480
 acaccccagg gaggagctgc cctcagccc caccctctc ctgccttcag cccagccttc 540
 gacaacctct attactggga ccaggaccca ccagagcggg gggctccacc cagcaccttc 600
 aaagggacac ctacggcaga gaaccagag tacctgggtc tggacgtgcc a 651

<210> 27
 <211> 397
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> NY-ESO-IC tumor antigen

<400> 27
 Met Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp
 1 5 10 15
 Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly
 20 25 30
 Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
 35 40 45
 Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala Pro Arg Gly Pro
 50 55 60
 His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala
 65 70 75 80
 Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe
 85 90 95
 Ala Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp
 100 105 110
 Ala Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val
 115 120 125
 Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln
 130 135 140
 Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met
 145 150 155 160
 Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser
 165 170 175
 Gly Gln Arg Arg Gly Ala Gly Gly Met Val His His Arg His Arg Ser

	180		185		190
Ser Ser Thr Arg Ser Gly Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro					
195		200		205	
Ser Glu Glu Glu Ala Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala					
210		215		220	
Gly Ser Asp Val Phe Asp Gly Asp Leu Gly Met Gly Ala Ala Lys Gly					
225		230		235	240
Leu Gln Ser Leu Pro Thr His Asp Pro Ser Pro Leu Gln Arg Tyr Ser					
	245		250		255
Glu Asp Pro Thr Val Pro Leu Pro Ser Glu Thr Asp Gly Tyr Val Ala					
	260		265		270
Pro Leu Thr Cys Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro Asp Val					
	275		280		285
Arg Pro Gln Pro Pro Ser Pro Arg Glu Gly Pro Leu Pro Ala Ala Arg					
	290		295		300
Pro Ala Gly Ala Thr Leu Glu Arg Ala Lys Thr Leu Ser Pro Gly Lys					
305		310		315	320
Asn Gly Val Val Lys Asp Val Phe Ala Phe Gly Gly Ala Val Glu Asn					
	325		330		335
Pro Glu Tyr Leu Thr Pro Gln Gly Gly Ala Ala Pro Gln Pro His Pro					
	340		345		350
Pro Pro Ala Phe Ser Pro Ala Phe Asp Asn Leu Tyr Tyr Trp Asp Gln					
	355		360		365
Asp Pro Pro Glu Arg Gly Ala Pro Pro Ser Thr Phe Lys Gly Thr Pro					
	370		375		380
Thr Ala Glu Asn Pro Glu Tyr Leu Gly Leu Asp Val Pro					
385		390		395	

<210> 28

<211> 1191

<212> DNA

<213> Artificial Sequence

<220>

<223> NY-ESO-IC tumor antigen.

<400> 28

atgcaggccg	aaggccgggg	cacaggggggt	tcgacggggcg	atgctgatgg	cccaggaggc	60
cctggcattc	ctgatggccc	agggggcaat	gctggcgggc	caggagaggc	gggtgccacg	120
ggcggcagag	gtccccgggg	cgcaggggca	gcaaggccct	cggggccggg	aggaggcgcc	180
ccgcggggtc	gcgatggcgg	cgcggcttca	gggctgaatg	gatgctgcag	atgcggggcc	240
agggggccgg	agagccgcct	gcttgagttc	tacctcgcca	tgcctttcgc	gacacccatg	300
gaagcagagc	tggcccgcag	gagcctggcc	caggatgccc	caccgcttcc	cgtgccaggg	360
gtgcttctga	aggagtccac	tgtgtccggc	aacatactga	ctatccgact	gactgctgca	420
gaccaccgcc	aactgcagct	ctccatcagc	tcctgtctcc	agcagctttc	cctgttgatg	480
tggatcacgc	agtgttttct	gcccgtgttt	ttggctcagc	ctccctcagg	gcagaggcgc	540
ggcgtggggg	gcatgggtcca	ccacaggcac	cgcagctcat	ctaccaggag	tggcgggtggg	600
gacctgacac	tagggctgga	gccctctgaa	gaggaggccc	ccaggtctcc	actggcaccc	660
tccgaagggg	ctgggtccga	tgtatttgat	ggtgacctgg	gaatgggggc	agccaagggg	720
ctgcaaagcc	tccccacaca	tgaccccagc	cctctacagc	ggtacagtga	ggaccccaca	780
gtacccctgc	cctctgagac	tgatggctac	gttgcccccc	tgacctgcag	ccccagcct	840
gaatatgtga	accagccaga	tgttcggccc	cagccccctt	cgccccgaga	gggccctctg	900
cctgctgccc	gacctgctgg	tgccactctg	gaaagggcca	agactctctc	cccagggaag	960
aatggggctg	tcaaagacgt	ttttgccttt	gggggtgccg	tggagaaccc	cgagtacttg	1020
acaccccagg	gaggagctgc	ccctcagccc	caccctctct	ctgccttcag	cccagccttc	1080
gacaacctct	attactggga	ccaggaccca	ccagagcggg	gggctccacc	cagcaccttc	1140
aaagggacac	ctacggcaga	gaacccagag	tacctgggtc	tggacgtgcc	a	1191

<210> 29
 <211> 1179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SART-3-IC

<400> 29

Met	Ala	Thr	Ala	Ala	Glu	Thr	Ser	Ala	Ser	Glu	Pro	Glu	Ala	Glu	Ser	1	5	10	15
Lys	Ala	Gly	Pro	Lys	Ala	Asp	Gly	Glu	Glu	Asp	Glu	Val	Lys	Ala	Ala	20	25	30	
Arg	Thr	Arg	Arg	Lys	Val	Leu	Ser	Arg	Ala	Val	Ala	Ala	Ala	Thr	Tyr	35	40	45	
Lys	Thr	Met	Gly	Pro	Ala	Trp	Asp	Gln	Gln	Glu	Glu	Gly	Val	Ser	Glu	50	55	60	
Ser	Asp	Gly	Asp	Glu	Tyr	Ala	Met	Ala	Ser	Ser	Ala	Glu	Ser	Ser	Pro	65	70	75	80
Gly	Glu	Tyr	Glu	Trp	Glu	Tyr	Asp	Glu	Glu	Glu	Lys	Asn	Gln	Leu		85	90	95	
Glu	Ile	Glu	Arg	Leu	Glu	Glu	Gln	Leu	Ser	Ile	Asn	Val	Tyr	Asp	Tyr	100	105	110	
Asn	Cys	His	Val	Asp	Leu	Ile	Arg	Leu	Leu	Arg	Leu	Glu	Gly	Glu	Leu	115	120	125	
Thr	Lys	Val	Arg	Met	Ala	Arg	Gln	Lys	Met	Ser	Glu	Ile	Phe	Pro	Leu	130	135	140	
Thr	Glu	Glu	Leu	Trp	Leu	Glu	Trp	Leu	His	Asp	Glu	Ile	Ser	Met	Ala	145	150	155	160
Gln	Asp	Gly	Leu	Asp	Arg	Glu	His	Val	Tyr	Asp	Leu	Phe	Glu	Lys	Ala	165	170	175	
Val	Lys	Asp	Tyr	Ile	Cys	Pro	Asn	Ile	Trp	Leu	Glu	Tyr	Gly	Gln	Tyr	180	185	190	
Ser	Val	Gly	Gly	Ile	Gly	Gln	Lys	Gly	Gly	Leu	Glu	Lys	Val	Arg	Ser	195	200	205	
Val	Phe	Glu	Arg	Ala	Leu	Ser	Val	Gly	Leu	His	Met	Thr	Lys	Gly		210	215	220	
Leu	Ala	Leu	Trp	Glu	Ala	Tyr	Arg	Glu	Phe	Glu	Ser	Ala	Ile	Val	Glu	225	230	235	240
Ala	Ala	Arg	Leu	Glu	Lys	Val	His	Ser	Leu	Phe	Arg	Arg	Gln	Leu	Ala	245	250	255	
Ile	Pro	Leu	Tyr	Asp	Met	Glu	Ala	Thr	Phe	Ala	Glu	Tyr	Glu	Glu	Trp	260	265	270	
Ser	Glu	Asp	Pro	Ile	Pro	Glu	Ser	Val	Ile	Gln	Asn	Tyr	Asn	Lys	Ala	275	280	285	
Leu	Gln	Gln	Leu	Glu	Lys	Tyr	Lys	Pro	Tyr	Glu	Glu	Ala	Leu	Leu	Gln	290	295	300	
Ala	Glu	Ala	Pro	Arg	Leu	Ala	Glu	Tyr	Gln	Ala	Tyr	Ile	Asp	Phe	Glu	305	310	315	320
Met	Lys	Ile	Gly	Asp	Pro	Ala	Arg	Ile	Gln	Leu	Ile	Phe	Glu	Arg	Ala	325	330	335	
Leu	Val	Glu	Asn	Cys	Leu	Val	Pro	Asp	Leu	Trp	Ile	Arg	Tyr	Ser	Gln	340	345	350	
Tyr	Leu	Asp	Arg	Gln	Leu	Lys	Val	Lys	Asp	Leu	Val	Leu	Ser	Val	His	355	360	365	
Asn	Arg	Ala	Ile	Arg	Asn	Cys	Pro	Trp	Thr	Val	Ala	Leu	Trp	Ser	Arg				

370	375	380
Tyr Leu Leu Ala Met Glu Arg His Gly Val Asp His Gln Val Ile Ser		
385	390	395
Val Thr Phe Glu Lys Ala Leu Asn Ala Gly Phe Ile Gln Ala Thr Asp		
405	410	415
Tyr Val Glu Ile Trp Gln Ala Tyr Leu Asp Tyr Leu Arg Arg Arg Val		
420	425	430
Asp Phe Lys Gln Asp Ser Ser Lys Glu Leu Glu Glu Leu Arg Ala Ala		
435	440	445
Phe Thr Arg Ala Leu Glu Tyr Leu Lys Gln Glu Val Glu Glu Arg Phe		
450	455	460
Asn Glu Ser Gly Asp Pro Ser Cys Val Ile Met Gln Asn Trp Ala Arg		
465	470	475
Ile Glu Ala Arg Leu Cys Asn Asn Met Gln Lys Ala Arg Glu Leu Trp		
485	490	495
Asp Ser Ile Met Thr Arg Gly Asn Ala Lys Tyr Ala Asn Met Trp Leu		
500	505	510
Glu Tyr Tyr Asn Leu Glu Arg Ala His Gly Asp Thr Gln His Cys Arg		
515	520	525
Lys Ala Leu His Arg Ala Val Gln Cys Thr Ser Asp Tyr Pro Glu His		
530	535	540
Val Cys Glu Val Leu Leu Thr Met Glu Arg Thr Glu Gly Ser Leu Glu		
545	550	555
Asp Trp Asp Ile Ala Val Gln Lys Thr Glu Thr Arg Leu Ala Arg Val		
565	570	575
Asn Glu Gln Arg Met Lys Ala Ala Glu Lys Glu Ala Ala Leu Val Gln		
580	585	590
Gln Glu Glu Glu Lys Ala Glu Gln Arg Lys Arg Ala Arg Ala Glu Lys		
595	600	605
Lys Ala Leu Lys Lys Lys Lys Lys Ile Arg Gly Pro Glu Lys Arg Gly		
610	615	620
Ala Asp Glu Asp Asp Glu Lys Glu Trp Gly Asp Asp Glu Glu Glu Gln		
625	630	635
Pro Ser Lys Arg Arg Arg Val Glu Asn Ser Ile Pro Ala Ala Gly Glu		
645	650	655
Thr Gln Asn Val Glu Val Ala Ala Gly Pro Ala Gly Lys Cys Ala Ala		
660	665	670
Val Asp Val Glu Pro Pro Ser Lys Gln Lys Glu Lys Ala Ala Ser Leu		
675	680	685
Lys Arg Asp Met Pro Lys Val Leu His Asp Ser Ser Lys Asp Ser Ile		
690	695	700
Thr Val Phe Val Ser Asn Leu Pro Tyr Ser Met Gln Glu Pro Asp Thr		
705	710	715
Lys Leu Arg Pro Leu Phe Glu Ala Cys Gly Glu Val Val Gln Ile Arg		
725	730	735
Pro Ile Phe Ser Asn Arg Gly Asp Phe Arg Gly Tyr Cys Tyr Val Glu		
740	745	750
Phe Lys Glu Glu Lys Ser Ala Leu Gln Ala Leu Glu Met Asp Arg Lys		
755	760	765
Ser Val Glu Gly Arg Pro Met Phe Val Ser Pro Cys Val Asp Lys Ser		
770	775	780
Lys Asn Pro Asp Phe Lys Val Phe Arg Tyr Ser Thr Ser Leu Glu Lys		
785	790	795
His Lys Leu Phe Ile Ser Gly Leu Pro Phe Ser Cys Thr Lys Glu Glu		
805	810	815
Leu Glu Glu Ile Cys Lys Ala His Gly Thr Val Lys Asp Leu Arg Leu		
820	825	830

Val	Thr	Asn	Arg	Ala	Gly	Lys	Pro	Lys	Gly	Leu	Ala	Tyr	Val	Glu	Tyr
		835					840					845			
Glu	Asn	Glu	Ser	Gln	Ala	Ser	Gln	Ala	Val	Met	Lys	Met	Asp	Gly	Met
		850					855					860			
Thr	Ile	Lys	Glu	Asn	Ile	Ile	Lys	Val	Ala	Ile	Ser	Asn	Pro	Pro	Gln
					870						875				880
Arg	Lys	Val	Pro	Glu	Lys	Pro	Glu	Thr	Arg	Lys	Ala	Pro	Gly	Gly	Pro
					885					890					895
Met	Leu	Leu	Pro	Gln	Thr	Tyr	Gly	Ala	Arg	Gly	Lys	Gly	Arg	Thr	Gln
			900					905					910		
Leu	Ser	Leu	Leu	Pro	Arg	Ala	Leu	Gln	Arg	Pro	Ser	Ala	Ala	Ala	Pro
			915					920					925		
Gln	Ala	Glu	Asn	Gly	Pro	Ala	Ala	Ala	Pro	Ala	Val	Ala	Ala	Pro	Ala
			930					935					940		
Ala	Thr	Glu	Ala	Pro	Lys	Met	Ser	Asn	Ala	Asp	Phe	Ala	Lys	Leu	Phe
					950					955					960
Leu	Arg	Gly	Ala	Gly	Gly	Met	Val	His	His	Arg	His	Arg	Ser	Ser	Ser
					965					970					975
Thr	Arg	Ser	Gly	Gly	Gly	Asp	Leu	Thr	Leu	Gly	Leu	Glu	Pro	Ser	Glu
			980					985						990	
Glu	Glu	Ala	Pro	Arg	Ser	Pro	Leu	Ala	Pro	Ser	Glu	Gly	Ala	Gly	Ser
			995					1000						1005	
Asp	Val	Phe	Asp	Gly	Asp	Leu	Gly	Met	Gly	Ala	Ala	Lys	Gly	Leu	Gln
			1010					1015					1020		
Ser	Leu	Pro	Thr	His	Asp	Pro	Ser	Pro	Leu	Gln	Arg	Tyr	Ser	Glu	Asp
					1030						1035				1040
Pro	Thr	Val	Pro	Leu	Pro	Ser	Glu	Thr	Asp	Gly	Tyr	Val	Ala	Pro	Leu
					1045					1050					1055
Thr	Cys	Ser	Pro	Gln	Pro	Glu	Tyr	Val	Asn	Gln	Pro	Asp	Val	Arg	Pro
					1060					1065					1070
Gln	Pro	Pro	Ser	Pro	Arg	Glu	Gly	Pro	Leu	Pro	Ala	Ala	Arg	Pro	Ala
					1075										1080
Gly	Ala	Thr	Leu	Glu	Arg	Ala	Lys	Thr	Leu	Ser	Pro	Gly	Lys	Asn	Gly
					1090					1095					1100
Val	Val	Lys	Asp	Val	Phe	Ala	Phe	Gly	Gly	Ala	Val	Glu	Asn	Pro	Glu
					1110					1115					1120
Tyr	Leu	Thr	Pro	Gln	Gly	Gly	Ala	Ala	Pro	Gln	Pro	His	Pro	Pro	Pro
					1125					1130					1135
Ala	Phe	Ser	Pro	Ala	Phe	Asp	Asn	Leu	Tyr	Tyr	Trp	Asp	Gln	Asp	Pro
					1140					1145					1150
Pro	Glu	Arg	Gly	Ala	Pro	Pro	Ser	Thr	Phe	Lys	Gly	Thr	Pro	Thr	Ala
					1155					1160					1165
Glu	Asn	Pro	Glu	Tyr	Leu	Gly	Leu	Asp	Val	Pro					
					1170					1175					

<210> 30
 <211> 3537
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> SART-3-IC

<400> 30	
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aaggctgacg gagaggagga tgaggttaag gcggctagga caaggagaaa ggtgttatcg	120
cgggctgtgg ccgctgcgac atacaagacc atggggccag cgtgggatca gcaggaggaa	180

ggcgtgagcg	agagcgatgg	ggatgagtag	gccatggctt	cctccgcgga	gagctcccc	240
ggggagtag	agtgggaata	tgacgaagag	gaggagaaaa	accagctgga	gattgagaga	300
ctggaggagc	agttgtctat	caacgtctat	gactacaact	gccatgtgga	cttgatcaga	360
ctgctcaggc	tggaagggga	gcttaccaag	gtgaggatgg	cccgccagaa	gatgagtga	420
atctttccct	tgactgaaga	gctctggctg	gagtggctgc	atgacgagat	cagcatggcc	480
caggatggcc	tgacagaga	gcacgtgtat	gacctctttg	agaaagccgt	gaaggattac	540
atctgtccta	acatttggt	agagtatggc	cagtactcag	ttggtgggat	tggtcagaaa	600
ggtggccttg	agaaagtctg	ctccgtgttt	gaaagggctc	tctcgtctgt	tggtttacat	660
atgaccaaag	gactcgccct	ctgggaggct	taccgagagt	ttgaaagtgc	gattgtggaa	720
gctgctcggc	ttgagaaagt	ccacagtctt	ttccggcgac	agttggcgat	cccactctat	780
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